

**AMENDMENTS TO THE CLAIMS:**

Please amend the claims as shown below. A complete listing of the claims, including their current status identifier, is set forth below.

1. (Original) A method of identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell, the method comprising

(i) identifying a set of regions of genomic DNA to which the protein of interest is bound in the cell;

(ii) identifying candidate DNA-binding sites in the identified regions of genomic DNA, wherein a candidate DNA-binding site comprises a sequence corresponding to a DNA-sequence motif for the protein of interest;

(iii) determining if the candidate DNA-binding sites are conserved in an equivalent genomic region in one or more species different from the species from which the cell is obtained, wherein a candidate DNA-binding site that is conserved in at least one of the different species is a biologically-active DNA-binding site.

2. (Original) The method of claim 1, wherein step (i) further comprises identifying a DNA sequence motif for the protein from the set of regions of genomic DNA.

3. (Original) The method of claim 2, wherein the DNA-sequence motif is enriched by a statistically-significant amount in the set of regions of genomic DNA relative to a suitable control.

4-6. (Canceled)

7. (Original) The method of claim 3, wherein the suitable control comprises a set of genomic regions which are bound by a mutant form of the protein of interest in the cell.

8. (Original) The method of claim 1, wherein the regions of genomic DNA comprise promoter regions.

9- 11. (Canceled)

12. (Original) The method of claim 2, wherein a candidate DNA-binding site is conserved if the equivalent genomic region in at least one different species comprises a nucleic acid sequence that matches the DNA-sequence motif for the protein of interest.

13- 15. (Canceled)

16. (Currently amended) The method of claim 1, wherein the candidate DNA-binding site is less ~~that~~ **than** 20 bp in length.

17. (Original) The method of claim 1, wherein the DNA-sequence motif is degenerate in at least one position.

18. (Canceled)

19. (Original) The method of claim 1, wherein step (iii) comprises determining if the candidate DNA-binding sites are conserved in equivalent genomic regions in two or more different species.

20-23. (Canceled)

24. (Original) The method of claim 1, wherein the set of biologically-active DNA-binding sites comprises one or more biologically-active DNA-binding sites.

25. (Canceled)

26. (Original) The method of claim 1, wherein two regions of genomic DNA are equivalent if they both comprise a sequence of at least one orthologous gene.

27. (Canceled)

28. (Original) The method of claim 1, wherein the cell is an eukaryotic cell.

29-35. (Canceled)

36. (Original) A method of identifying an agent which alters the set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell, the method comprising

(i) contacting an experimental cell with a candidate agent;

(ii) identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of the cell of step (i) according to the method of claim 2, thereby generating an experimental set of biologically-active DNA-binding sites;

(iii) comparing

(1) the experimental set of biologically-active DNA-binding sites to

(2) a control set of biologically-active DNA-binding sites for the protein of interest;

wherein a candidate agent is identified if the experimental set and the control set differ.

37. (Canceled)

38. (Original) A method of identifying a pathway that is transcriptionally regulated by a protein of interest in a cell, the method comprising

(i) identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of the cell according to the method of claim 2; and

(ii) identifying at least two candidate genes likely to be regulated by binding of the protein of interest to the set of biologically-active DNA-binding sites identified in (i); wherein a pathway that is transcriptionally regulated by the protein of interest is identified if at least two candidate genes are members of the same pathway.

39. (Canceled)

40. (Canceled)

41. (Original) The method of claim 38, wherein the pathway is a gene expression pathway.

42-44. (Canceled)

45. (Previously presented) A method of identifying two sets of conditions in which a protein of interest differentially binds to the genome of a cell, the method comprising:

(i) identifying, according to the method of claim 1,

(1) a first set of biologically-active DNA-binding sites for the protein of interest in the genome of a cell, wherein the cell is exposed to a first set of conditions; and

(2) identifying a second set of biologically-active DNA-binding sites for the protein of interest in the genome of a cell, wherein the cell is exposed to a second set of conditions; and

(iii) comparing the first set of biologically-active DNA-binding sites to the second set of biologically-active DNA-binding sites and determining if the two sets differ.

46. (Previously presented) A method of identifying a property of a gene product of a gene of interest that correlates with the binding activity of a polypeptide encoded by the gene of interest to the genome of a cell, the method comprising

(i) identifying two sets of conditions in which a protein of interest differentially binds to the genome of the cell according to the method of claim 45;

(ii) determining a property of a gene product of the gene of interest in (a) a cell exposed to the first set of conditions; and in (b) a cell exposed to the second set of conditions; and

(iii) determining if at least one property of the gene product differs in the two cells of step (ii), thereby identifying a property that correlates with the binding activity of a gene of interest to the genome of a cell.

47. (Original) A method of identifying a property of a gene product of a gene of interest that correlates with the binding activity of a polypeptide encoded by the gene of interest to the genome of a cell, the method comprising

(i) identifying an agent which alters the set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell according to the method of claim 36;

(ii) determining a property of a gene product of the gene of interest in (a) a cell contacted with the agent; and in (b) a cell not contacted with the agent; and  
(iii) determining if at least one property of the gene product differs in the two cells of step (ii), thereby identifying a property that correlates with the binding activity of a gene of interest to the genome of a cell.

48. (Previously presented) The method of claim 46, wherein the property is selected from the group consisting of a protein modification, expression level, enzymatic activity and intracellular localization.

49-59. (Canceled).

60. (Currently amended) A method of identifying two cell genotypes in which a protein of interest differentially binds to the genome of a cell, the method comprising:

(i) identifying a first set of biologically-active DNA-binding sites for the protein of interest in the genome of a cell of a first genotype;  
(ii) identifying a second set of biologically-active DNA-binding sites for the protein of interest in the genome of a cell of a second genotype;  
(iii) comparing the first set of biologically-active DNA-binding sites to the second set of biologically-active DNA-binding sites and determining if the two sets differ, **thereby identifying two cell genotypes in which said protein of interest differentially binds to the genome.**